

#3

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/870,937

DATE: 06/19/2001

TIME: 12:09:10

Input Set : A:\514.app.txt

Output Set: N:\CRF3\06192001\I870937.raw

ENTERED

3 <110> APPLICANT: Wu, Bin
 4 Seeley, Todd
 5 Williams, Lewis T.
 10 <120> TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING NEOPLASTIC DISEASE
 USING
 11 CHEMOTHERAPY AND RADIATION SENSITIZERS
 13 <130> FILE REFERENCE: 200130.514/PP-01623.002
 C--> 15 <140> CURRENT APPLICATION NUMBER: US/09/870,937
 16 <141> CURRENT FILING DATE: 2001-05-30
 18 <160> NUMBER OF SEQ ID NOS: 12
 20 <170> SOFTWARE: FastSEQ for Windows Version 3.0
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 25
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Artificial Sequence
 27 <220> FEATURE:
 28 <223> OTHER INFORMATION: Antisense Oligonucleotide
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 34 <211> LENGTH: 25
 35 <212> TYPE: DNA
 36 <213> ORGANISM: Artificial Sequence
 38 <220> FEATURE:
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 41 <400> SEQUENCE: 2
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 47 <213> ORGANISM: Artificial Sequence
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 52 <400> SEQUENCE: 3
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 58 <213> ORGANISM: Artificial Sequence
 60 <220> FEATURE:
 61 <223> OTHER INFORMATION: Antisense Oligonucleotide
 63 <400> SEQUENCE: 4
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 67 <211> LENGTH: 25
 68 <212> TYPE: DNA
 69 <213> ORGANISM: Artificial Sequence
 71 <220> FEATURE:

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72 <223> OTHER INFORMATION: Antisense Oligonucleotide
74 <400> SEQUENCE: 5
75   gggtagcact ggcttgtcca cagga                                25
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79 <212> TYPE: DNA
80 <213> ORGANISM: Artificial Sequence
82 <220> FEATURE:
83 <223> OTHER INFORMATION: Antisense Oligonucleotide
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86   aggacacctg ttcggtcacg atggg                                25
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89 <211> LENGTH: 27
90 <212> TYPE: DNA
91 <213> ORGANISM: Artificial Sequence
93 <220> FEATURE:
94 <223> OTHER INFORMATION: Primer for PCR amplification of KIAA0175
96 <400> SEQUENCE: 7
97   gggatcagg aggcagcggc ttaaggg                                27
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101 <212> TYPE: DNA
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104 <220> FEATURE:
105 <223> OTHER INFORMATION: PRIMER for PCR amplification of KIAA0175
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111 <211> LENGTH: 2470
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113 <213> ORGANISM: Homo sapien
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116   ttggcgggcg gaagcggcca caaccggcg atcgaaaaga ttcttaggaa cgccgtacca    60
117   gccgcgtctc tcaggacagc aggccctgt ccttctgtcg ggcgccgtc agccgtgcc    120
118   tccgccctc aggttctttt tctaattcca aataaacttg caagaggact atgaaagatt    180
119   atgatgaact tctcaaatat tatgaattac atgaaactat tgggacaggg ggctttgcaa    240
120   aggtcaaaact tgccctgccat atccttactg gagagatggg agctataaaa atcatggata    300
121   aaaacacact agggagtgat ttgccccgga tcaaaacgga gattgaggcc ttgaagaacc    360
122   tgagacatca gcatatatgt caactctacc atgtgctaga gacagccaac aaaatattca    420
123   tggttcttga gtaactgcct ggaggagagc tgtttgacta tataatttcc caggatcgcc    480
124   tgtcagaaga ggagaccggg gttgtcttcc gtcagatagt atctgctgtt gcttatgtgc    540
125   acagccaggg ctatgctcac agggacctca agccagaaaa tttgctgttt gatgaatata    600
126   ataaattaaa gctgattgac tttggtctct gtgcataaac caagggtaac aaggattacc    660
127   atctacagac atgctgtggg agtctggctt atgcagcacc tgagttaata caaggcaaat    720
128   catatcttgg atcagaggca gatgtttgga gcatgggcat actgtttatat gttcttatgt    780
129   gtggatttct accattttgat gatgataatg taatggcttt atacaagaag attatgagag    840
130   gaaaatatga tgttcccaag tggctctctc ccagtagcat tctgcttctt caacaaatgc    900
131   tgcagggtga cccaaagaaa cggatttcta tgaaaaatct attgaaccat ccctggatca    960
132   tgcaagatta caactatcct gttgagtggc aaagcaagaa tcctttttatt cacctcgatg   1020

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133 atgattgcgt aacagaactt tctgtacatc acagaaacaa caggcaaaca atggaggatt 1080
134 taattttcact gtggcagtat gatcacctca cggctaccta tcttctgctt ctaggccaaga 1140
135 aggctcgggg aaaaccagtt cgtttaaggc tttcttcttt ctctgtgga caagccagtg 1200
136 ctaccccatc cacagacatc aagtcaaata attggagtct ggaagatgtg accgcaagtg 1260
137 ataaaaatta tgtggcggga ttaatagact atgattggtg tgaagatgat ttatcaacag 1320
138 gtgctgctac tccccgaaca tcacagttta ccaagtactg gacagaatca aatggggtgg 1380
139 aatctaaatc attaaactcca gccttatgca gaacacctgc aaataaatta aagaacaaag 1440
140 aaaatgtata tactcctaag tctgctgtaa agaatgaaga gtactttatg tttcctgagc 1500
141 caaagactcc agttaataag aaccagcata agagagaaat actcactacg ccaaactcgtt 1560
142 acactacacc ctcaaaagct agaaaccagt gcctgaaaga aactccaatt aaaataccag 1620
143 taaattcaac aggaacagac aagttaatga cagggtgcat tagccctgag aggcggtgcc 1680
144 gctcagtgga attggatctc aaccaagcac atatggagga gactccaaaa agaaagggag 1740
145 ccaaagtgtt tgggagcctt gaaaggggtt tggataaggt tatcactgtg ctaccagga 1800
146 gcaaaaggaa gggttctgcc agagacgggc ccagaagact aaagcttcac tataatgtga 1860
147 ctacaactag attagtgaat ccagatcaac tgttgaatga aataatgtct attcttccaa 1920
148 agaagcatgt tgactttgta caaaagggtt atacactgaa gtgtcaaaca cagtcagatt 1980
149 ttgggaaagt gacaatgcaa tttgaattag aagtgtgcca gcttcaaaaa cccgatgtgg 2040
150 tgggtatcag gaggcagcgg cttaaggcgg atgcctgggt ttacaaaaga ttagtggag 2100
151 acatcctatc tagctgcaag gtataattga tggattcttc catcctgcgg gatgagtgtg 2160
152 ggtgtgatac agcctacata aagactgtta tgatcgcttt gattttaaag ttcattggaa 2220
153 ctaccaactt gtttctaaag agctatctta agaccaatat ctctttgttt ttaaacaaaa 2280
154 gatattatct tgtgtatgaa tctaaatcaa gccatctgt cattatgtta ctgtcttttt 2340
155 taatcatgtg gttttgtata ttaataattg ttgactttct tagattcact tccatagtgt 2400
156 aatgtaagct cttaactatg tctctttgta atgtgtaatt tctttctgaa ataaaacct 2460
157 ttgtgaatat 2470
159 <210> SEQ ID NO: 10
160 <211> LENGTH: 651
161 <212> TYPE: PRT
162 <213> ORGANISM: Homo sapien
164 <400> SEQUENCE: 10
165 Met Lys Asp Tyr Asp Glu Leu Leu Lys Tyr Tyr Glu Leu His Glu Thr
166 1 5 10 15
167 Ile Gly Thr Gly Gly Phe Ala Lys Val Lys Leu Ala Cys His Ile Leu
168 20 25 30
169 Thr Gly Glu Met Val Ala Ile Lys Ile Met Asp Lys Asn Thr Leu Gly
170 35 40 45
171 Ser Asp Leu Pro Arg Ile Lys Thr Glu Ile Glu Ala Leu Lys Asn Leu
172 50 55 60
173 Arg His Gln His Ile Cys Gln Leu Tyr His Val Leu Glu Thr Ala Asn
174 65 70 75 80
175 Lys Ile Phe Met Val Leu Glu Tyr Cys Pro Gly Gly Glu Leu Phe Asp
176 85 90 95
177 Tyr Ile Ile Ser Gln Asp Arg Leu Ser Glu Glu Glu Thr Arg Val Val
178 100 105 110
179 Phe Arg Gln Ile Val Ser Ala Val Ala Tyr Val His Ser Gln Gly Tyr
180 115 120 125
181 Ala His Arg Asp Leu Lys Pro Glu Asn Leu Leu Phe Asp Glu Tyr His
182 130 135 140
183 Lys Leu Lys Leu Ile Asp Phe Gly Leu Cys Ala Lys Pro Lys Gly Asn

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184 145          150          155          160
185 Lys Asp Tyr His Leu Gln Thr Cys Cys Gly Ser Leu Ala Tyr Ala Ala
186          165          170          175
187 Pro Glu Leu Ile Gln Gly Lys Ser Tyr Leu Gly Ser Glu Ala Asp Val
188          180          185          190
189 Trp Ser Met Gly Ile Leu Leu Tyr Val Leu Met Cys Gly Phe Leu Pro
190          195          200          205
191 Phe Asp Asp Asp Asn Val Met Ala Leu Tyr Lys Lys Ile Met Arg Gly
192          210          215          220
193 Lys Tyr Asp Val Pro Lys Trp Leu Ser Pro Ser Ser Ile Leu Leu Leu
194          225          230          235          240
195 Gln Gln Met Leu Gln Val Asp Pro Lys Lys Arg Ile Ser Met Lys Asn
196          245          250          255
197 Leu Leu Asn His Pro Trp Ile Met Gln Asp Tyr Asn Tyr Pro Val Glu
198          260          265          270
199 Trp Gln Ser Lys Asn Pro Phe Ile His Leu Asp Asp Asp Cys Val Thr
200          275          280          285
201 Glu Leu Ser Val His His Arg Asn Asn Arg Gln Thr Met Glu Asp Leu
202          290          295          300
203 Ile Ser Leu Trp Gln Tyr Asp His Leu Thr Ala Thr Tyr Leu Leu Leu
204          305          310          315          320
205 Leu Ala Lys Lys Ala Arg Gly Lys Pro Val Arg Leu Arg Leu Ser Ser
206          325          330          335
207 Phe Ser Cys Gly Gln Ala Ser Ala Thr Pro Phe Thr Asp Ile Lys Ser
208          340          345          350
209 Asn Asn Trp Ser Leu Glu Asp Val Thr Ala Ser Asp Lys Asn Tyr Val
210          355          360          365
211 Ala Gly Leu Ile Asp Tyr Asp Trp Cys Glu Asp Asp Leu Ser Thr Gly
212          370          375          380
213 Ala Ala Thr Pro Arg Thr Ser Gln Phe Thr Lys Tyr Trp Thr Glu Ser
214          385          390          395          400
215 Asn Gly Val Glu Ser Lys Ser Leu Thr Pro Ala Leu Cys Arg Thr Pro
216          405          410          415
217 Ala Asn Lys Leu Lys Asn Lys Glu Asn Val Tyr Thr Pro Lys Ser Ala
218          420          425          430
219 Val Lys Asn Glu Glu Tyr Phe Met Phe Pro Glu Pro Lys Thr Pro Val
220          435          440          445
221 Asn Lys Asn Gln His Lys Arg Glu Ile Leu Thr Thr Pro Asn Arg Tyr
222          450          455          460
223 Thr Thr Pro Ser Lys Ala Arg Asn Gln Cys Leu Lys Glu Thr Pro Ile
224          465          470          475          480
225 Lys Ile Pro Val Asn Ser Thr Gly Thr Asp Lys Leu Met Thr Gly Val
226          485          490          495
227 Ile Ser Pro Glu Arg Arg Cys Arg Ser Val Glu Leu Asp Leu Asn Gln
228          500          505          510
229 Ala His Met Glu Glu Thr Pro Lys Arg Lys Gly Ala Lys Val Phe Gly
230          515          520          525
231 Ser Leu Glu Arg Gly Leu Asp Lys Val Ile Thr Val Leu Thr Arg Ser
232          530          535          540

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233 Lys Arg Lys Gly Ser Ala Arg Asp Gly Pro Arg Arg Leu Lys Leu His
 234 545 550 555 560
 235 Tyr Asn Val Thr Thr Thr Arg Leu Val Asn Pro Asp Gln Leu Leu Asn
 236 565 570 575
 237 Glu Ile Met Ser Ile Leu Pro Lys Lys His Val Asp Phe Val Gln Lys
 238 580 585 590
 239 Gly Tyr Thr Leu Lys Cys Gln Thr Gln Ser Asp Phe Gly Lys Val Thr
 240 595 600 605
 241 Met Gln Phe Glu Leu Glu Val Cys Gln Leu Gln Lys Pro Asp Val Val
 242 610 615 620
 243 Gly Ile Arg Arg Gln Arg Leu Lys Gly Asp Ala Trp Val Tyr Lys Arg
 244 625 630 635 640
 245 Leu Val Glu Asp Ile Leu Ser Ser Cys Lys Val
 246 645 650

249 <210> SEQ ID NO: 11

250 <211> LENGTH: 25

251 <212> TYPE: DNA

252 <213> ORGANISM: Artificial Sequence

254 <220> FEATURE:

255 <223> OTHER INFORMATION: Primer for PCR amplification of KIAA0175

257 <400> SEQUENCE: 11

258 tctgctgctg tcgacaacga gtgctc

25

262 <210> SEQ ID NO: 12

263 <211> LENGTH: 25

264 <212> TYPE: DNA

265 <213> ORGANISM: Artificial Sequence

267 <220> FEATURE:

268 <223> OTHER INFORMATION: Primer for PCR amplification of KIAA0175

270 <400> SEQUENCE: 12

271 ccatagtgag gttgcatctg gtgcc

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/870,937

DATE: 06/19/2001

TIME: 12:09:11

Input Set : A:\514.app.txt

Output Set: N:\CRF3\06192001\I870937.raw

L:15 M:270 C: Current Application Number differs, Wrong Format